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## RAW SEQUENCE LISTING

DATE: 02/04/2002

PATENT APPLICATION: US/10/007,521

TIME: 11:36:15

Input Set : N:\Crf3\RULE60\10007521.raw

Output Set: N:\CRF3\02042002\J007521.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Schulein, Martin  
 6 Andersen, Lene N.  
 7 Lassen, Soren F.  
 8 Kauppinen, Markus S.  
 9 Lange, Lene  
 10 Nielsen, Ruby I.  
 11 Ihara, Michiko  
 12 Takagi, Shinobu

ENTERED

14 (ii) TITLE OF INVENTION: Novel Endoglucanases

16 (iii) NUMBER OF SEQUENCES: 109

18 (iv) CORRESPONDENCE ADDRESS:

- 19 (A) ADDRESSEE: Novo Nordisk of North America, Inc.  
 20 (B) STREET: 405 Lexington Avenue, 64th Floor  
 21 (C) CITY: New York  
 22 (D) STATE: New York  
 23 (E) COUNTRY: United States of America  
 24 (F) ZIP: 10174-6401

26 (v) COMPUTER READABLE FORM:

- 27 (A) MEDIUM TYPE: Floppy disk  
 28 (B) COMPUTER: IBM PC compatible  
 29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

32 (vi) CURRENT APPLICATION DATA:

- C--> 33 (A) APPLICATION NUMBER: US/10/007,521  
 C--> 34 (B) FILING DATE: 10-Dec-2001  
 35 (C) CLASSIFICATION:

38 (vii) PRIOR APPLICATION DATA:

- 39 (A) APPLICATION NUMBER: US/08/651,136  
 40 (B) FILING DATE: 21-MAY-1996

43 (viii) ATTORNEY/AGENT INFORMATION:

- 44 (A) NAME: Lambiris, Elias J.  
 45 (B) REGISTRATION NUMBER: 33,728  
 46 (C) REFERENCE/DOCKET NUMBER: 4366.200-US

48 (ix) TELECOMMUNICATION INFORMATION:

- 49 (A) TELEPHONE: 212-867-0123  
 50 (B) TELEFAX: 212-878-9655

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

- 56 (A) LENGTH: 960 base pairs  
 57 (B) TYPE: nucleic acid  
 58 (C) STRANDEDNESS: single

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59      (D) TOPOLOGY: linear
61      (ii) MOLECULE TYPE: cDNA
63      (ix) FEATURE:
64          (A) NAME/KEY: CDS
65          (B) LOCATION: 113..787
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 AAAGAAAGGC TCTCTGCTGT CGTCGCTCTC GTCGCTCTCG TCGGCATCCT CCATCCGTCC      60
71 GCCTTTGATA ACCCGCTCCC CGACTCAGTC AAGACGACGC ATACTTGCA CC ATG      115
72                                     Met
73                                     1
75 CAT CTC TCC GCC ACC ACC GGG TTC CTC GCC CTC CCG GTC CTG GCC CTG      163
76 His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala Leu
77          5          10          15
79 GAC CAG CTC TCG GGC ATC GGC CAG ACG ACC CGG TAC TGG GAC TGC TGC      211
80 Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys Cys
81          20          25          30
83 AAG CCG AGC TGC GCC TGG CCC GGC AAG GGC CCC TCG TCT CCG GTG CAG      259
84 Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val Gln
85          35          40          45
87 GCC TGC GAC AAG AAC GAC AAC CCG CTC AAC GAC GGC GGC TCC ACC CGG      307
88 Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr Arg
89          50          55          60          65
91 TCC GGC TGC GAC GCG GGC GGC AGC GCC TAC ATG TGC TCC TCC CAG AGC      355
92 Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln Ser
93          70          75          80
95 CCC TGG GCC GTC AGC GAC GAG CTG TCG TAC GGC TGG GCG GCC GTC AAG      403
96 Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val Lys
97          85          90          95
99 CTC GCC GGC AGC TCC GAG TCG CAG TGG TGC TGC GCC TGC TAC GAG CTG      451
100 Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu Leu
101          100          105          110
103 ACC TTC ACC AGC GGG CCG GTC GCG GGC AAG AAG ATG ATT GTG CAG GCG      499
104 Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln Ala
105          115          120          125
107 ACC AAC ACC GGT GGC GAC CTG GGC GAC AAC CAC TTT GAC CTG GCC ATC      547
108 Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala Ile
109          130          135          140          145
111 CCC GGT GGC GGT GTC GGT ATT TTC AAC GCC TGC ACC GAC CAG TAC GGC      595
112 Pro Gly Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr Gly
113          150          155          160
115 GCT CCC CCG AAC GGC TGG GGC GAC CGC TAC GGC GGC ATC CAT TCC AAG      643
116 Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser Lys
117          165          170          175
119 GAA GAG TGC GAA TCC TTC CCG GAG GCC CTC AAG CCC GGC TGC AAC TGG      691
120 Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn Trp
121          180          185          190
123 CGC TTC GAC TGG TTC CAA AAC GCC GAC AAC CCG TCG GTC ACC TTC CAG      739
124 Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe Gln
125          195          200          205

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```

127 GAG GTG GCC TGC CCG TCG GAG CTC ACG TCC AAG AGC GGC TGC TCC CGT      787
128 Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser Arg
129 210      215      220      225
131 TAAGAGGGGAA GAGAGGGGGC TGGAAGGACC GAAAGATTCA ACCTCTGCTC CTGCTGGGGA      847
133 AGCTCGGGCG CGAGTGTGAA ACTGGTGTAA ATATTGTGC ACACACAAGC TACTACAGTC      907
135 CGTCTCGCCG TCCGGCTAAC TAGCCTTGCT GCGGATCTGT CCAAAAAAAAA AAA      960
138 (2) INFORMATION FOR SEQ ID NO: 2:
140 (i) SEQUENCE CHARACTERISTICS:
141 (A) LENGTH: 225 amino acids
142 (B) TYPE: amino acid
143 (D) TOPOLOGY: linear
145 (ii) MOLECULE TYPE: protein
147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
149 Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala
150 1      5      10      15
152 Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys
153      20      25      30
155 Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val
156      35      40      45
158 Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr
159      50      55      60
161 Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln
162 65      70      75      80
164 Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val
165      85      90      95
167 Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu
168      100      105      110
170 Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln
171      115      120      125
173 Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala
174      130      135      140
176 Ile Pro Gly Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr
177 145      150      155      160
179 Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser
180      165      170      175
182 Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn
183      180      185      190
185 Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe
186      195      200      205
188 Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser
189      210      215      220
191 Arg
192 225
195 (2) INFORMATION FOR SEQ ID NO: 3:
197 (i) SEQUENCE CHARACTERISTICS:
198 (A) LENGTH: 894 base pairs
199 (B) TYPE: nucleic acid
200 (C) STRANDEDNESS: single
201 (D) TOPOLOGY: linear

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```

203      (ii) MOLECULE TYPE: cDNA
205      (ix) FEATURE:
206          (A) NAME/KEY: CDS
207          (B) LOCATION: 1..891
209      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
211 ATG CAT CTC TCC GCC ACC ACC GGG TTC CTC GCC CTC CCG GTC CTG GCC      48
212 Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala
W--> 213      230      235      240
215 CTG GAC CAG CTC TCG GGC ATC GGC CAG ACG ACC CGG TAC TGG GAC TGC      96
216 Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys
W--> 217      245      250      255
219 TGC AAG CCG AGC TGC GCC TGG CCC GGC AAG GGC CCC TCG TCT CCG GTG      144
220 Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val
W--> 221      260      265      270
223 CAG GCC TGC GAC AAG AAC GAC AAC CCG CTC AAC GAC GGC GGC TCC ACC      192
224 Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr
W--> 225      275      280      285
227 CGG TCC GGC TGC GAC GCG GGC GGC AGC GCC TAC ATG TGC TCC TCC CAG      240
228 Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln
W--> 229 290      295      300      305
231 AGC CCC TGG GCC GTC AGC GAC GAG CTG TCG TAC GGC TGG GCG GCC GTC      288
232 Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val
W--> 233      310      315      320
235 AAG CTC GCC GGC AGC TCC GAG TCG CAG TGG TGC TGC GCC TGC TAC GAG      336
236 Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu
W--> 237      325      330      335
239 CTG ACC TTC ACC AGC GGG CCG GTC GCG GGC AAG AAG ATG ATT GTG CAG      384
240 Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln
W--> 241      340      345      350
243 GCG ACC AAC ACC GGT GGC GAC CTG GGC GAC AAC CAC TTT GAC CTG GCC      432
244 Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala
W--> 245      355      360      365
247 ATC CCC GGT GGC GGT GTC GGT ATT TTC AAC GCC TGC ACC GAC CAG TAC      480
248 Ile Pro Gly Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr
W--> 249 370      375      380      385
251 GGC GCT CCC CCG AAC GGC TGG GGC GAC CGC TAC GGC GGC ATC CAT TCC      528
252 Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser
W--> 253      390      395      400
255 AAG GAA GAG TGC GAA TCC TTC CCG GAG GCC CTC AAG CCC GGC TGC AAC      576
256 Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn
W--> 257      405      410      415
259 TGG CGC TTC GAC TGG TTC CAA AAC GCC GAC AAC CCG TCG GTC ACC TTC      624
260 Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe
W--> 261      420      425      430
263 CAG GAG GTG GCC TGC CCG TCG GAG CTC ACG TCC AAG AGC GGC TGC TCC      672
264 Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser
W--> 265      435      440      445
267 CGT CCC TCC AGC AGC ACC AGC TCT CCG GTC AAC CAG CCT ACC AGC ACC      720
268 Arg Pro Ser Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr

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W--> 269 450          455          460          465
      271 AGC ACC ACG TCC ACC TCC ACC ACC TCG AGC CCG CCA GTC CAG CCT ACG      768
      272 Ser Thr Thr Ser Thr Ser Thr Thr Ser Ser Pro Pro Val Gln Pro Thr
W--> 273          470          475          480
      275 ACT CCC AGC GGC TGC ACT GCT GAG AGG TGG GCT CAG TGC GGC GGC AAT      816
      276 Thr Pro Ser Gly Cys Thr Ala Glu Arg Trp Ala Gln Cys Gly Gly Asn
W--> 277          485          490          495
      279 GGC TGG AGC GGC TGC ACC ACC TGC GTC GCT GGC AGC ACT TGC ACG AAG      864
      280 Gly Trp Ser Gly Cys Thr Thr Cys Val Ala Gly Ser Thr Cys Thr Lys
W--> 281          500          505          510
      283 ATT AAT GAC TGG TAC CAT CAG TGC CTG TAG      894
      284 Ile Asn Asp Trp Tyr His Gln Cys Leu
W--> 285          515          520
      288 (2) INFORMATION FOR SEQ ID NO: 4:
      290 (i) SEQUENCE CHARACTERISTICS:
      291 (A) LENGTH: 297 amino acids
      292 (B) TYPE: amino acid
      293 (D) TOPOLOGY: linear
      295 (ii) MOLECULE TYPE: protein
      297 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
      299 Met His Leu Ser Ala Thr Thr Gly Phe Leu Ala Leu Pro Val Leu Ala
      300 1 5 10 15
      302 Leu Asp Gln Leu Ser Gly Ile Gly Gln Thr Thr Arg Tyr Trp Asp Cys
      303 20 25 30
      305 Cys Lys Pro Ser Cys Ala Trp Pro Gly Lys Gly Pro Ser Ser Pro Val
      306 35 40 45
      308 Gln Ala Cys Asp Lys Asn Asp Asn Pro Leu Asn Asp Gly Gly Ser Thr
      309 50 55 60
      311 Arg Ser Gly Cys Asp Ala Gly Gly Ser Ala Tyr Met Cys Ser Ser Gln
      312 65 70 75 80
      314 Ser Pro Trp Ala Val Ser Asp Glu Leu Ser Tyr Gly Trp Ala Ala Val
      315 85 90 95
      317 Lys Leu Ala Gly Ser Ser Glu Ser Gln Trp Cys Cys Ala Cys Tyr Glu
      318 100 105 110
      320 Leu Thr Phe Thr Ser Gly Pro Val Ala Gly Lys Lys Met Ile Val Gln
      321 115 120 125
      323 Ala Thr Asn Thr Gly Gly Asp Leu Gly Asp Asn His Phe Asp Leu Ala
      324 130 135 140
      326 Ile Pro Gly Gly Gly Val Gly Ile Phe Asn Ala Cys Thr Asp Gln Tyr
      327 145 150 155 160
      329 Gly Ala Pro Pro Asn Gly Trp Gly Asp Arg Tyr Gly Gly Ile His Ser
      330 165 170 175
      332 Lys Glu Glu Cys Glu Ser Phe Pro Glu Ala Leu Lys Pro Gly Cys Asn
      333 180 185 190
      335 Trp Arg Phe Asp Trp Phe Gln Asn Ala Asp Asn Pro Ser Val Thr Phe
      336 195 200 205
      338 Gln Glu Val Ala Cys Pro Ser Glu Leu Thr Ser Lys Ser Gly Cys Ser
      339 210 215 220
      341 Arg Pro Ser Ser Ser Thr Ser Ser Pro Val Asn Gln Pro Thr Ser Thr

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## VERIFICATION SUMMARY

DATE: 02/04/2002

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Input Set : N:\CrF3\RULE60\10007521.raw

Output Set: N:\CRF3\02042002\J007521.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:391 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:395 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:431 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:548 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:552 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:568 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7

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Input Set : N:\Crf3\RULE60\10007521.raw

Output Set: N:\CRF3\02042002\J007521.raw

L:572 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:576 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:580 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:584 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:3513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79  
L:3529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80  
L:3545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81  
L:3561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82  
L:3577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83  
L:3907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:105  
L:3922 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106  
L:3937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:107  
L:3952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:108  
L:3967 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109